TABLE 1 Exon-Intron Boundary Sequences of the Human alpha-7 nAChR Subunit Gene

Exon	Exon	CDNA	splice		splice	Intron	Intron Size
Number	length(bp)	position	acceptor	flanking exon sequence	donor	number	approximate (Kb)
1	55	1-55		CTG CAC G	GTAAAGCCAC	1	0.3
2	140	56-195	TCTCCTTAAG	TG TCCGAC GTG	GTGAGTCCCG	2	Unknown
				v s d v			
3	45	196-240	TTTTTTGAAG	GAT GAGCAA ATG	GTAAGTTAAG	3	9.0
				DE Q M			
4	110	241-350	TGTGTGTCAG	TCT TGGAAC AG	GTAAGCATAT	4	Unknown
5	80	351-430	CTGTTTCTAG		GTAAGCTGCA	5	4.0
6	168	431-598	ACCCACACAG	A D P P GC ATACTA GTG G	GTAAGCCATG	6	1.0
7	195	599-793	CCCTATGGAG	G I L V GA ATCTCC CTG G	GTAAGCGCCC	7	1.0
8	87	794-880	TATGTTTTAG	G I S L GG ATATTG ATA G G I L I	GTAAGGCAAG	8	3.5
9	110	881-990	CTCTCCACAG	CC CAGAAG TGG	GTACGTTCCT	9	5.0
10	519	991-1509	GTCTCCCCAG	A Q K W ACC AGA T R			

4,50

FIGURE 2

TABLE 2 Sequence Variants Identified in Full-Length and Duplicated Genomic Clones

176630		6GT	8GT		6GT	6GT	T.J.	8.0.T	8GT	8GT	8GT	8GT	8GT	8GT	8GT	8GT		8GT
7 10	1335																	Ę
EXO	13	2/2			U	U	2/2)	U	U	U	U	U	O	U	U		
0																		
EXON	1269						T/7	,										
		2/2			U	U			U	U	U	U	U	U	U	U		U
					Ø	Ą												
EXON 7	069	G/A					G/A											
									ပ	ც	b	ပ	b	U	U	ပ		ŋ
					٤٦	٤٠												
EXON 7	654	C/T					C/T											
									U	U	υ	U	U	U	U	υ		ပ
	498				-TG	-TG												
EXON	+/- 497-	+TG	-TG				+TG	-TG										
	'								+TG	+TG	+TG	+TG	+TG	+TG	+TG	+TG		+TG
EXONS	CONT.	5-10	1-10		5-10	6-10	5-10	1-10	1-10	1-10	1-10	1-10	1-10	1-10	1-10	1-10		1-10
	A NO.	CHR15	HYBRID	YAC	D-948a10	D-853b12	D/F	969611	F-134h10	F-776a12	F-791e6	F-811b6	F-953g6	F-859c11	F-810f11	F-801e1	BAC	F-467018

DNA	Control #		EXON 6 +/- 497-498	498	1 44	EXON 7	7		EXON 690	7		EXON 10 1269	0	च	EXON 10 1335	0
Control Genomic DNA	43	10	33	-/-	c/c 5	C/C C/T 5 38	T/T 0	و/و 0	G/A 43	T/T G/G G/A A/A C/C 0 43 0 6	9	C/T 36	1/1	C/C C/T 24 19	C/T 19	1/T 0

TABLE 3 Expression Analysis of Sequence Variants

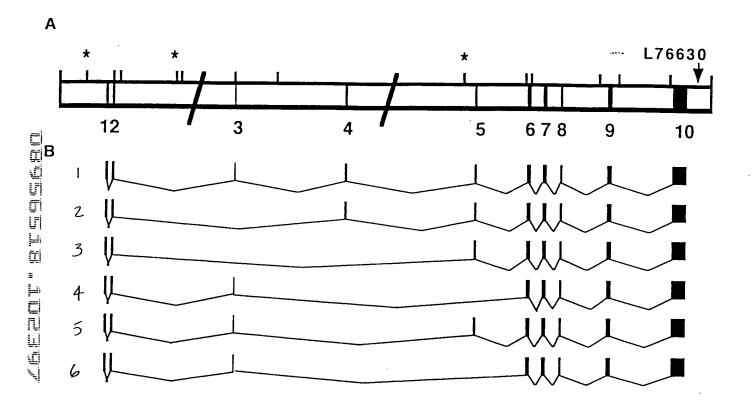
	Bas	es 497	498	E	Base 65	. .	Ε	Base 69	0	Ε	Base 93	3	В	ase 129	96	В	ase 13	35
Subj	DNA	1-10 cDNA	5-10 cDNA															
SL061	+/-	+	+/-	CT	C	СТ	GA	G	GA	G	G	G	CT	СТ	СТ	С	С	С
SL084	+	+	+	С	С	С	GA	G	GA	G	G	G	CT	С	CT	C	С	С
SL111	+/-	+	+/-	CT	С	СТ	GA	G	GA	G	G	G	CT	CT	СТ	CT	СТ	CT
SL097	+_	+ -	+	CT	С	CT	GA	G	GA	G	G	G	CT	С	CT	С	С	С
SL089	+	+	+	С	С	С	GA	GA	GA	GA	GA	GA	CT	CT	CT	С	С	С
SHSY	+/-	+	+/-	CT	С	СТ	GA	GA	GA	GA	GA	GA	С	С	С	С	С	С

-392	agaacgcaag	ggagaggtag	agcetggeet	tgggcagccc	ctggdctggc	cagaggcgcg	aggccgagag
				Al	2-2		
-322	cccgctcggt	ggagactggg	ggtggaggtg	cccggagcgt	acccagegee	gggagtacct	cccgctcaca
-252	cctcgggctg	cagttccctg	ggtggccgcc	gagacgctgg	cccgggctgg	agggatggcg	gggcggggac
-182	gggggcgggg	geggggeteg	tcacgtggag	aggcgcgcgg	gggcgggggg	ggcgggggcg	cacacccaac
			REB		Sp1		
-112	tccttaaagg	cgcgcgagcc	gageggegag	gtgcctctgt	ggccgcaggc	gcaggcccgg	gcgacagccg
						2 33 33	
-42	agacgtggag	cgcgccggct	cgctgcagct	ccgggactca	acATGCGCTG	CTCGCCGGGA	GGCGTCTGGC
					Met		
+29	TGGCGCTGGC	CGCGTCGCTC	CTGCACGata	aaqccac			
			3	2			

FIGURE 5

CENTROMERE	1ERE																							F	TELOMERE	E RE	٠			
				ALPEA-7		SEQUENCE	TENC	Ħ			l		ALP	alpha-7		3EQU	SEQUENCE	M												
PAC	82 QX	D1551043	00,	\$16630	EXON 9	Kron 8	1 V	-3.	D153	D155165	D1551031	8X0.30	EXOL 10				EXON S			OF	D1551360		D155144 D155144	. 9 "	D155995 D1551007	.9 ⁹⁵				
PAC		,	1	,	٠ ا	',		,	,		٠		٠ ا					.	:	*				1						
25919		ŧ	ŧ	•	•						•	•	•		ì	1		t			•				•	•				
BAC																					*									
467018		•	r	•	•	1		•		ı	•	+	+	+	+	+	+ 1	+	+	+		+	1		ı	. 1				
YAC																														
948410	1730	+	+	+	+	+	+	+	+	+	•	1	•	•		'		•							•	•				
853512	190	+	+	+	+	+	+	+		•	•	ı	1				1	•					4	1	•	٠				
89526	1580	1	+	+	•	,		•			ı	•	٠			'	•					1				1				
969511	1030	•	•	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	•		,		·	•	•			
776a12	1640	1	•	1	•	'	'	•		+	+	+	+	+	+	+	+	+	+	+	٠				•	1				
79106	1170	ı	•	•		,	,	•		+	+	+	+	+	+	+	+	+	+	+	•		+	+		•				
81156	1060	•	1	•	•	'		•	1	•	+	+	+	+	+	+	+	+		+	•		,	,	1	ı				
95346	1720	•	•	•	•	•		•			•	+	+	+	+	+	+	+	+	+	*					. 1				
134110	N . A .	•	•	•	•	'		•	1		+	+	+	+	+	+	+	+	+	+	•		ı		ı	•				
859c11	1330	ı	•	•	•	,		•				+	+	+	+	+	+	+	+	+	r		,		ı	ı				
810£11	940	•	•	1		•		1	ı		1	+	+	+		+	+	+	+	+			+		1	•				
80101	1630	ı	•	'	•	,		•	,		•	+	+	+	+	+	+	+	+	+	•		+	+	+	+				
966a4	1500	1	•	•	•	,		•		,	•	•	•		,	ı	•				•		+	+	ı	•				
76428	740	ı	•	•	•	1	1	•	Ç	1	•	•	•	t			•				٠			+	+	+				
82292	1280	ı	ı	•	•	1		,	1	ι		•	•			,	•				٠	ı		+	٠	+				
•	-	_																												

	1						
EXON D	CAGGCCGCCA	CATAGCTCCC	GCCAAGTCCT	CGGTGCCCCT	TGCCATTTTC	CAGCCGCGTC	CCACGAGGGT
297bp	CACGGCGGCG	GGGAGAGGTG	GAGCCGCGAG	AGCTCGGCCG	GGGGCCCGC	CTGGTGGCCG	CGGCCATGAC
	AGCGGCTCGG	GACTGGCTCC	TTTTCCGCGC	CCCTCCCGCC	GGAGGTGAGG	GGAAGATGTC	CATGTCAGGG
	TTCAAGGCCA	AACCGAAGTT	ACTGGCCTCT	ATCTTCCAGG	AGAACCAGGA	GCCACAGCCG	CGGCTCACGC
	CCCACCGCAA	CATTAAGgtg	agtcgcc	•			
!		297			•		
		298					
ежом с	ctc	atttcagATT	ACAAGTGGAC	ACCTGAGTCA	GCAGGACCTG	GAATCCCAGA	TGAGAGAGCT
125bp	TATCTACACG	ACTCAGATCT	TGTTGTCACC	CCCATTATTG	ACAATCCAAA	GGTGCAGAAA	GCACTCTGAC
	A Agtgagttg	ta					
T]	422						
		423			•		
EXON B	ttaaccac	agataatgaa	ACAACCACCA	TCGGTTAAAT	TTGATGCAAA	AATATTGCAT	CTACCAGCAT
6 20 bp	TTTCAGgtag	gatcat					
æ	· 486						
		487					
EXON A	ttta	ttctagTTCC	AATTGCTAAT	CCAGCATTTG	TGGATAGCTG	CAAACTGCGA	TATgtaagta
47bp	aca					•	533
L							
T		534					
EXON 5	ctgtttc	tagTGCTGAT	GAGCGCTTTG	ACGCCACATT	CCACACTAAC	GTGTTGGTGA	ATTCTTCTGG
qď08		GCATTGCCAG	TACCTGCCTC	CAGgtaagctg 613	ca		
		614		013			
TTYON C			CAACACIIIIICC	mooma cameo			
EXON 6	acccaca	cagGCATATT	CAAGAGTTCC	TGCTACATCG 640			
27bp				640			



- 61 aggccgagag cccgctcggt ggagactggg ggtggaggtg cccggagcgt acccagcgcc
- 121 gggagtacct cccgctcaca cctcgggctg cagttccctg ggtggccgcc gagacgctgg
- 181 cccgggctgg agggatggcg gggcggggac gggggcgggg gcggggctcg tcacgtggag
- 241 aggegegeg gggegggeg ggegggggeg egegeeegge teettaaagg egegegagee
- 301 gagcggcgag gtgcctctgt ggccgcaggc gcaggcccgg gcgacagccg agacgtggag
- 361 egegeegget egetgeaget eegggaetea ac

1 agccetttcc caggeggtag egggggcagt ggtgetgttg ecettttaaa etgeggettg

- 61 acgggageeg egeeteetgt eggtggagte ggttataaag ggageageee egeaggeege
- 121 cacatagete eegecaagte eteggtgeee ettgeeattt teeageegeg eteceaegag
- 181 ggtcacggcg gcggggagag gtggagccgc gagagctcgg ccgggggccc cgcctggtgg
- 241 ccgcggccat gacagcggct cgggactggc tccttttccg cgcccctccc gccggaggtg
- 301 aggggaagat gtccatgtca gggttcaagg ccaaaccgaa gttactggcc tctatcttcc
- 361 aggagaacca ggagccacag ccgcggctca cgccccaccg caacattaag attacaagtg
- 421 gacacetgag teageaggae etggaateee agatgagaga gettatetae aegaeteaga
- 481 tettgttgte acceccatta ttgacaatee aaaggtgeag aaageaetet gacaatteea
- 541 attgctaatc cagcatttgt ggatagctgc aaactgcgat attgctgatg agcgctttga
- 601 egecacatte cacactaaeg tgttggtgaa ttettetggg cattgecagt acetgeetee
- 661 aggcatattc aagagttcct gctacatcg

- 1 caggeegeca catageteec gecaagteet eggtgeeect tgecatttte cageegeget
- 61 cccacgaggg tcacggcggc ggggagaggt ggagccgcga gagctcggcc gggggccccg
- 121 cctggtggcc gcggccatga cagcggctcg ggactggctc cttttccgcg cccctcccgc
- 181 cggaggtgag gggaagatgt ccatgtcagg gttcaaggcc aaaccgaagt tactggcctc
- 241 tatetteeag gagaaceagg ageeacagee geggeteaeg eeceaeegea acattaagat
- 301 tacaagtgga cacctgagtc agcaggacct ggaatcccag atgagagagc ttatctacac
- 361 gactcagatc ttgttgtcac ccccattatt gacaatccaa aggtgcagaa agcactctga
- 421 caaataatga aacaaccacc atcggttaaa tttgatgcaa aaatattgca tctaccagca
- 481 ttttcagttc caattgctaa tccagcattt gtggatagct gcaaactgcg atattgctga
- 541 tgagegettt gaegeeacat teeacactaa egtgttggtg aattettetg ggeattgeea
- 601 gtacetgeet ecaggeatat teaagagtte etgetacate g